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☐ 1: J Biochem (Tokyo) 1999 Jun;125(6):1086-93

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Sequence of the *V. parahaemolyticus* gene for cytoplasmic N, N'-diacetylchitobiase and homology with related enzymes.

Wu MH, Laine RA.

Department of Biological Sciences, Louisiana State University and A&M College and The LSU Agricultural Center, Baton Rouge, LA 70803, USA.

The nucleotide sequence of the gene encoding the cytoplasmic N, N'-diacetylchitobiase [EC 3.2.1.14] from *Vibrio parahaemolyticus* (ATCC #27969) has been determined. The deduced peptide sequence of this unusual beta-hexosaminidase surprisingly shows minimum evolutionary relationship to two other reported N, N'-diacetylchitobioses from vibrios, except in highly conserved regions which are also homologous to lysosomal beta-hexosaminidases from eukaryotes including humans. In contrast, the two other beta-hexosaminidases from vibrios with reported sequences are much more closely related to each other. This novel 85 kDa cytoplasmic glycosyl hydrolase with restricted specificity participates in the high level utilization of chitin-derived 2-deoxy-2-acetamido-D-glucose (GlcNAc) by vibrios as one of two parallel pathways for the metabolism of N,N'-diacetylchitobiose [Bassler, B.L., Yu, C., Lee, Y.C., and Roseman, S. (1991) J. Biol. Chem. 266, 24276-24286]. These pathways use chitin-binding proteins for the adherence of the bacterial chitinase to the substrate, and an extracellular chitinase and a periplasmic chitodextrinase to produce N,N'-diacetylchitobiose. The *V. parahaemolyticus* cytoplasmic N,N'-diacetylchitobiase reported herein appears to be a unique protein, lacking a signal sequence, and genetically distant from other known chitinoclastic beta-N,N'-diacetylhexosaminidases. This is consistent with its limited substrate specificity to small GlcNAc terminated oligosaccharides and its cytoplasmic rather than periplasmic localization.

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